



FIG. 1E.

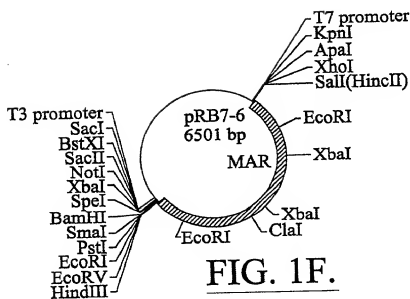
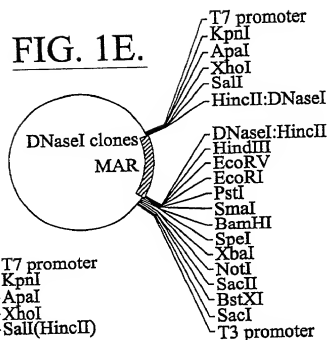


FIG. 1F.

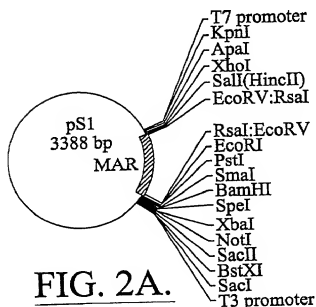


FIG. 2A.

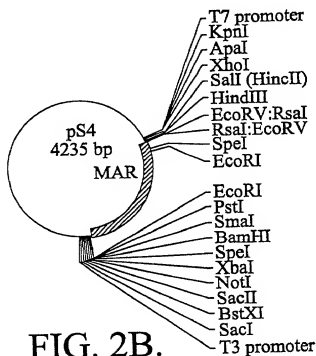


FIG. 2B.

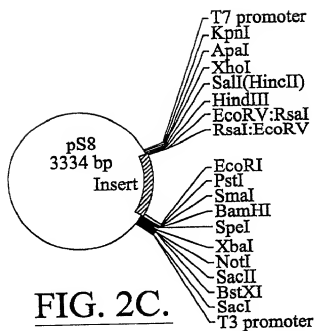


FIG. 2C.

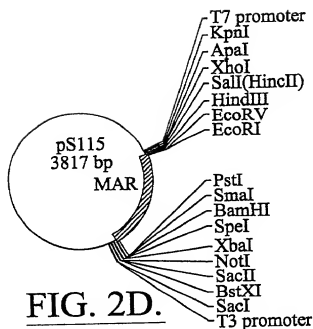


FIG. 2D.

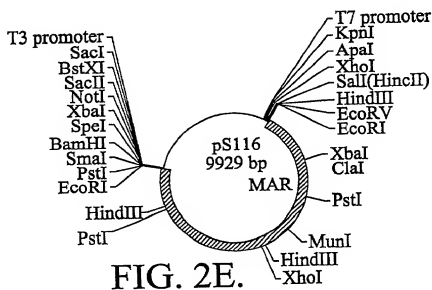


FIG. 2E.

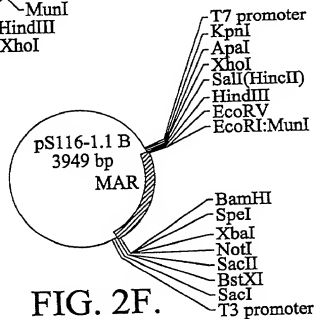


FIG. 2F.

FIG. 2G.

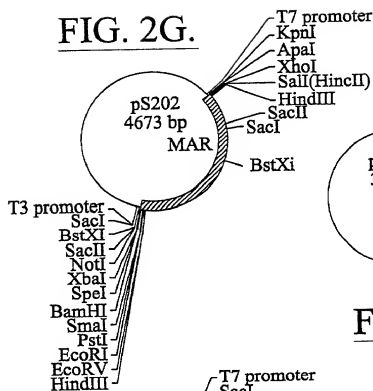


FIG. 2H.

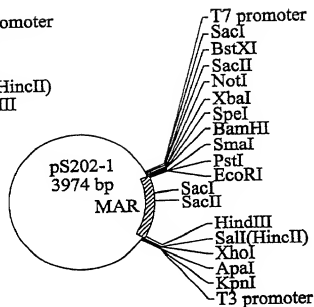


FIG. 2I.

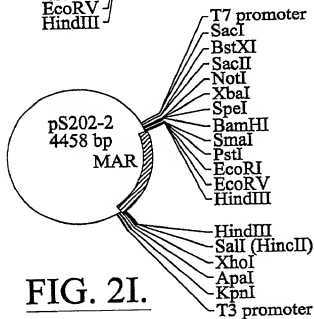
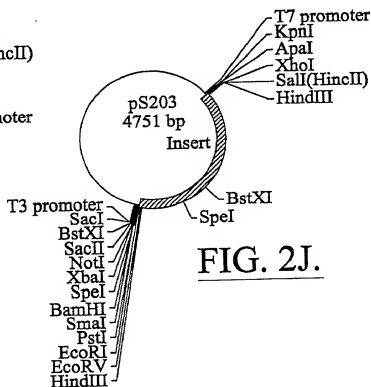
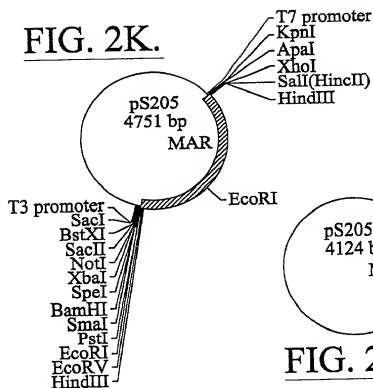


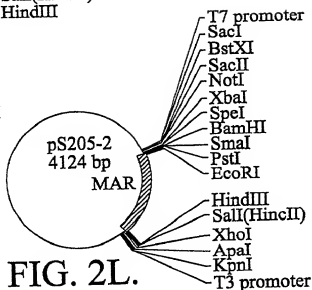
FIG. 2J.



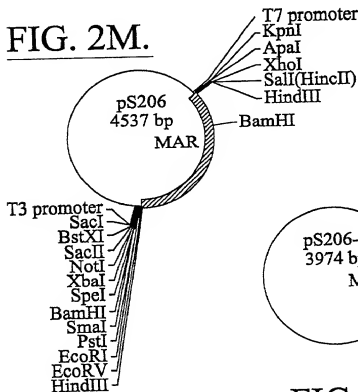
**FIG. 2K.**



**FIG. 2L.**



**FIG. 2M.**



**FIG. 2N.**

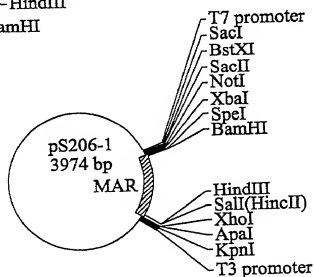


FIG. 2O.

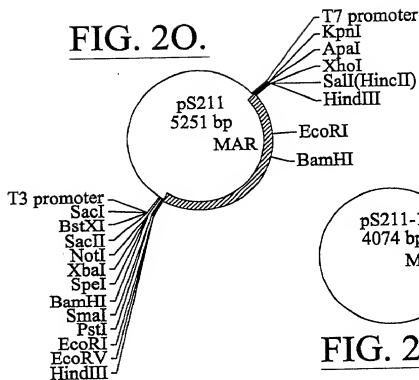


FIG. 2P.

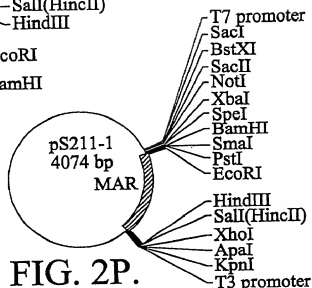


FIG. 2Q.

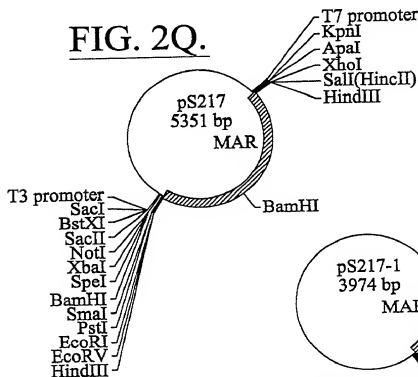
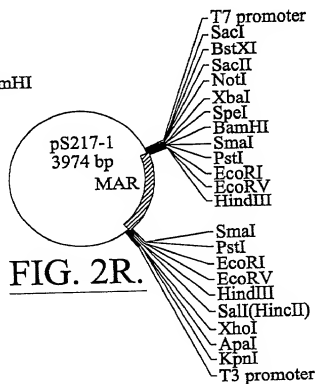
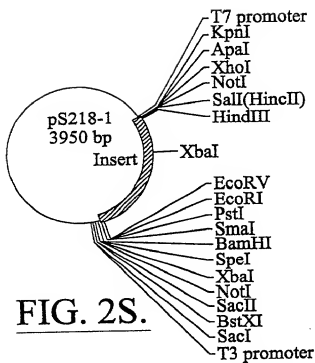
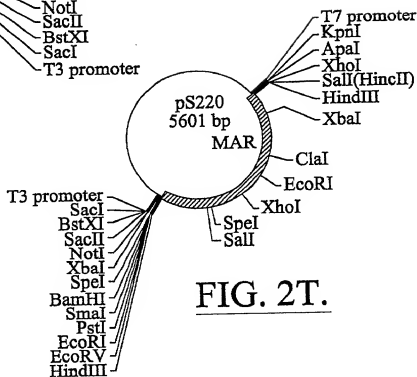


FIG. 2R.

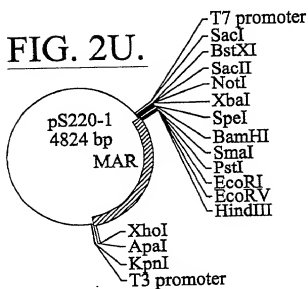




**FIG. 2S.**

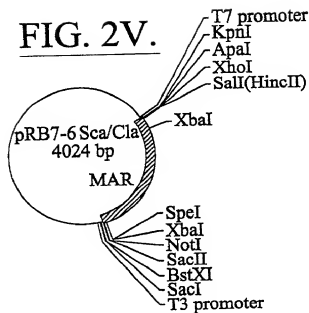


**FIG. 2T.**

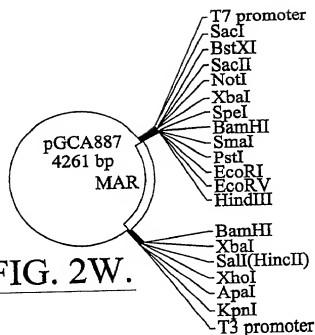


**FIG. 2U.**

**FIG. 2V.**



**FIG. 2W.**





# pS1 (SEQ ID NO:1)

1 GATACGTAAA CAACGTGTAT CCAGTAAGTA TCAAGCCTAA TCTCGAAGTG  
 51 GTAGAGACGA GATGACCGAC TTTGACACTC ACTATGGGTC AATAATAATA  
 101 ACTGAAATAA AACTAAGATA TTTAAACCAA CATGATTAC AGAATTTACA  
 151 ATAATTTATT TAATCAGCAG AAATAATCAA ATTTCTTCAA ATGTAACAAT  
 201 TCTCAATATA TTAATTTAAAT TCCTTCAATT CAAATAATTT CTAATTTATC  
 251 AATTAACCT CATTACAGG AGTAACAATT AATTCCTTAA CAAGCAAGAA  
 301 TAATAATTCA TTAAATTCCA AGGATTTTTC AATTTATTAA TTAGCTTCAC  
 351 AACCTGAAAT AAATTATTAA AGTATCGTGT AATTATTAIT ATTAAGCACG  
 401 ATTTCTGCCG AGGACATACG GCCCGATCCA GAGTATC

# pS4 (SEQ ID NO:2)

1 GATACTAGAG TGGTGTATC AATCTTACT CGTATGAATT AATTAATTT  
 51 GTCTCTTATT TCTGTCCTAA GTCATATACA AGAAATGCTA ACTCCATCCG  
 101 TTTCAATCCC TATGACATAG TTTGATTTGA TTGAATTTGA AAATTTAAGA  
 151 AACAAAAGAT AATTTTTGTG ACTCATAATT TAGACATGTG TTATAAGACT  
 201 TTTCTCATGA ATTTTTTGA AACAAATGAT AATTTTTTGA ACTCATAATT  
 251 TAGACGTTTT ATAAAAATA CTAACGTGAT CTGGTTCAAT ATTTATGTGT  
 301 TATTCCTATA AAACCTCTGG ACTTATATTT TTAAATATTT CATATATTT  
 351 GGTATCGGTA TAAATTTTTT GTCACTTTTG GATGAAAGGG AAGTTTAAGT  
 401 AAATTTCTTT TTCCAAATTT AGAAAGTTAT AATATTCTTT TTAACGCC  
 451 CAAAAGAAA AATAAGCTAT TGATTATTAT AAGCCTAAAC CAAAAGATT  
 501 CTTTGACTAG TAGGAAGCCA TTTTAAAGTT AGGCGCCAAA ATTCAAGCC  
 551 AACGTGGGCA TATCTCCAAA CTGGCGGCTA CAGTATC

# pS8 (SEQ ID NO:3)

1 ACCGCTTTTA TTATTATTAT TTTTACCGAG AATTACAACA TCATGAAAAT  
 51 ACATCTCGAA CCACGTGACA TCAATGCACC CGCGGTTATT GACATATTTT  
 101 AACTCTGTTG AGATTGGAT TTGGGTCACA TAAATGTGCA CCCGAGTTTA  
 151 AGAGGATAAC ATTATTTAAAT ACGCGCCTAA AACGACTAGC GTATCATTAT  
 201 TTTGGGTAGG GCCGTGAAAT TTTGCTAAAC TGCCCATCCA GAAATCTAAG  
 251 TAATTTTACC AACACGTATA GAGGGCCCCA CAGCTTGTTG ATTTTGTGTT  
 301 GTCGAGGCTC GTCTCATTCA TTATTTTAA AAGGAATTG CAACGTCGTG  
 351 GAAATGCATC TCGAACCACG TCACAATCAA TGA

**FIG. 3.**

pS115 (SEQ ID NO:4)

1 GAATTCGATA GACTCACTTA AATATTAGAA GTGAATTACC TAGAGTTAGA  
 51 TCCAAACAA TTATCTTGCA CCTATCTAT CAACCCTTAT CTTTCCCAT  
 101 TGATTACTAC CTTGCTTACC TTGTACGA TTTCATTAG ACAATAACTT  
 151 TAGATTCTTA GTTAATTGCA GTTAGAAAT ATATTAAAT TCAATTGTTG  
 201 GATCATCTTG AATACCAATC AAGCTAGAAA ATACAAGAA ACTGTTAAAA  
 251 TCAATCCAT GTGGATACGA TATTATACTA TATTATATT GACTGTGAG  
 301 CATTATTAT GTGTGTTTTG TGCTCGTCAA AGTTTGCGT CGTGCCGAG  
 351 GATTGGCAAT CAATAGTGT TGAATAGTT TTTGGTGCTA ATTTAGGAAT  
 401 TAGGTTTTAT TTATTTATTT TTCTTTTCT TTCTTTTTC CTTTCTATT  
 451 TTATTTCTT TATTAGTTAA CTCTTTTCA AGATTTTTT TGTAGTACCT  
 501 AACCAAGTTAG AGAAGATACT GTAGATTTTG AACTCTAAAT GTTGTGAAGA  
 551 TGGAGTACAA CCAGCCTAAG AAAATATTTG AATAGTTAGC AGCTGAACAT  
 601 TATCGGCGT CGGTTATGCG GTTTAAATGC GGTGGAAGCA TCTACCACC  
 651 CAGCCTAAAG AAAATATTTT GAATAGTTAG CAGCTTGAAC ATTATCGGCG  
 701 GTCGGTTATG TGTTTTAAAT GCGGTGGAAA TCATCTACGG GCTAACTGTC  
 751 AAGCAGGTAT GTATCTTCC TATGTTTCGT ATTTTGAGGA GTCTCACTCT  
 801 GTTCTAGTT CGTACATGTA TGAGGAATCA TATGGGCACA ACTCTGACTC  
 851 TGGTTGGGAT GAATTC

pS116-1.1B (SEQ ID NO:5)

1 GAATTGTATT ATTGTTAGGT GGGAGAGATT TTTGACTATA TGGGTAAAAA  
 51 TCAGCGACAA AGGGCCAAAT ATACCTATTT ACTTTTAAAA ATAGTCTAAT  
 101 AATACCTCTC GTTATATTAT TAGGTTATCT ATACCTTTGC AGTCATATTT  
 151 TGGGTTCAAA TATACCCCTC ATTTAAACGG AGGGACACGT GTCATGCTCC  
 201 TGTTGGTCAA TTCTAAATAT CTCTAATTA ATTAAAAAGA CTCATTACCC  
 251 ATATCCGAAA AATATTTTTT AAAGCAATAT TTTTTATAA AAAATGGAAA  
 301 AACTGAAATT ATTTTACTA AAAATTGAAA AAAACGAAAA TAGTTTTTTT  
 351 TCAGTTTTTA CAAAAAACT ATTTTAGAAA AAATTGAAAA ATATTTTCTA  
 401 AAACAATGTT TTTGTAAAAA CTGAAAAAAA AGAAGCTGAA AATCAATTTT  
 451 CTAAAGCAAT TTTATTTGTA AAATCTGAAA AAAACTACTA AAAACTGAAA  
 501 AAATGAAAT ATTTTTTTT CTAATTTTTA CAAAAAAAC TGCTTTAAAA  
 551 AAAGCTGAAA ATATTTTCTA AAACAATATT TTTGTAAAAA CTAAAAAA  
 601 AATATTTCT TCTTTTTTC AGTTTTAGT TAAAAATATT TAAGTTTTTT  
 651 CCAGTTTTTA ATTACTTTAG AAAATTACTT TTCTGCTTTT TTTTCAGTTT  
 701 TTCAAAAAAT ATTATTTTAG AAAATATTTT TCAGTCTTTT AAAGCAGTTT  
 751 TTTTTTGTA AAACCTGAAA AACAATATT TCGTTTTTTT CAGTTTTTAG  
 801 TAAAAATTGT TTTTAGTTTT TTTCAGTTTT TACCAAAAAA AAAATTGCTT  
 851 TAGAAAAATTA TTTTTCGGGT ATGGGTAATG GGTCTTTTA ATTAATTAGG  
 901 AGATATTTTG AATTGATCAA TAGGACGATG ACACATGTCC CTCGGTTTAA  
 951 ATGAGGTGTA TATTGAATC CAAAGTAAGA CTGCAGCCCG GGGGATCC

FIG. 3. (continued)

pS202-1 (SEQ ID NO:6)

1 GAATTCGATA TGGCTTGTG GACAAGAATT AATGAATCAA TTGTGAAAAA  
 51 GTTGATGGAC ATATTGAAGG TAAATCATTA TACTATTTTT CTAAAACTC  
 101 TTTTAAATGT TCCCAATTA TCTGATTTC ATATTGCTCT TAAATGTCAC  
 151 TCAACCTTAG ATCAACAAAC ATATAACTTA CCCAGTACAT AAGAGATTGC  
 201 GGCATTATGG CTGGAAGAAA ATCCTAGAGA CACATCTGCA CCACATATTT  
 251 GAATTTATAC CCACAGTAAT AGAGCTCGGT TAGTACATTA TTATTATGGA  
 301 TGTTACGATC CGTTGCAGTA TCCATTATTA TTTTCCTTCG GTGAAAAATGG  
 351 ATGACATTGT GGAATTAATA AAATTATTCA GACAAAAAT TCGACGAAAC  
 401 GTAGAGCTTA CTGCGAACAT GAACAATTGC CAGTATATC AAATACGTGT  
 451 TCAGTTGATG GATTTCCTGA TATGGAAGAT GAATCACTAC AAAGAGGAAA  
 501 ACGAAAAAGA GATACAGTGT CTTGTCGAGA GTATTATTGT TACAAATTC  
 551 AACTAAGAAA TAATGAAACA AATGAAGTGT TACATTGTGG GAGAAATTTT  
 601 CAACAATTTA TAGTAGATAT ATATATATAA AGCTT

pS202-2 (SEQ ID NO:7)

1 AAGCTTGCAC GCCTACATCG TGGGATAATT TAGAAAAAGG AAAGGGTATA  
 51 TTGGATCCCC CTATCATTTG TGAAACAGGT AACCATACGA GAACCCCTTT  
 101 CGCTTCCTGA AAAATGTTAT ATATTGTTGT ACTCATATTT ATACACTATT  
 151 TATTATTAAT ATAACGATGC TTATTTTGCT TGGAGATTGG AGATTATCAC  
 201 AGCTTATTTA TCTTATATTG TATCTTATTA AACTTAAAAA CATAAATACT  
 251 ACGTGTCTTT TTAATTGGG ATCTATTAAG GGTTCGTGC ACGCTTTTAA  
 301 ACATCTTGGC TATTCGTITT ACCAGCTGCT ACCTTAGCCT GTATGCTTAC  
 351 ATCATCTCCT AATTTAGACA AAGGAAAGGG TATATTGGAC CCCCCCATC  
 401 ATTCGTGAAA CAGGTAACAA TACATTGAGA TTATACTCTT TTCAGAATGA  
 451 CATATTGTTT ATACATTACT GTAAATTGTG ACTATTGTGA TATTAGGGTC  
 501 CACATCGGGT ACATCTAACC TGCCTCATGT TATCTTGAACT ACTGTTCCAA  
 551 TCAAAGGTTT GCACAACTT AATGTTACAA TCATGTCCAC CATACGTATG  
 601 CCTTGGTGTCT CTTTTTTTTC CTAATGATAC TTCTTATATA TTCAGCTCAT  
 651 AGGCGGGCCA GAAAGGTGTG CCTGGTCACT AAAGAGCAAC GAAGTGAGTA  
 701 TGTGTCTCTA AAAAGGGTCC CACACTGTCA ATTCTGTCTAT CCAAAGAAGT  
 751 TTGAATATGA ACCTCCAGGA TTTTGTGTGA ACAGTGGTTC AATAAGGTTG  
 801 ACATCTCATA AAATGCCAAC TGAATTATCG GAGTTTACT TTGGAATATC  
 851 TGAAGAATCT GAAATTTTTC GAACCTATAT TAGAACATAC AATAACATGT  
 901 TTGCATTTAC TTCACTTGGT GTCAAGTATG ATAAAGAGCT AGCGAGAAGA  
 951 AATTGTGGTA TCTACACATT TAGAGTCCAG GGACAGATGT ATCATTTTAT  
 1001 AGATGATTTA GTTCCTTCCA ATGAAAAACC TAGGAATTTA TAGCTGTACT  
 1051 TCTACGATAA TGATAATGAA CTAGCCAAAT CAAGCTT

FIG. 3. (continued)

**pS205-2 (SEQ ID NO:8)**

1 GAATCTTCA GCCATTGTAC ATATAGTTGT GTATTAATGT TATTAATAAT  
51 GGATAATTAA ATATATACCT GGAATAAATA TACGATATTA TAATAGTGTG  
101 TAATTATATA TAAAAATTAT ACATAATATA ATGATGGTAT TTAATATAGC  
151 ATAAATTTGA ACGATCTGGA TTGATTTCTT GAATCAAAAT AGAGTTGTGT  
201 GAAAAGAAAA GAATGAGATG AAAAGCAAAG TATGAAGAGA TGAATTTGTG  
251 TTTTTTTTAT GGAGGAGGAA GGTTCCTAGT GATGGAATCA TCCCTGGTTT  
301 TCTTTAGCAC CAATGAAAGT AATGAACCCC CCCCAGGATA AAAAAAATAA  
351 AAAAAAAGG GAGAGAGAGT AGAATGGAAC GGCTAGGTGA AAGTATAGGA  
401 GTAGAAATTA GGTTTCAGGA GAGAAAAGGG GGGAAATTAA TTCCTAAATT  
451 AATGGGATTC TAATTTTAA ACTGTTTTGA AATATTTTAA AAGTAGTGTG  
501 ATTTATATTA TTAACTTTTA AAAAAAGTCA AACGAGGTAA AAATCCATG  
551 GGGGAAAAAT TAAATGGTTA GTCTTCTATA ATATTTTCAA CTCTGCTTAG  
601 CACTAAAAAT TAGTCTAAAA ATAACCTTAA ATTAGTGTAT CTAATTAAT  
651 TACTTCATCG AACAGGAGCA TTGGATTATC CCTCCAGAGT TACACAGGAA  
701 GCTT

**pS206-1 (SEQ ID NO:9)**

1 GGATCCAGCT ATTATTATAG CATGTGAGTT GTCCGTGAAC AGCTAATTTT  
51 TTACCACACC CAAATTCAAT ACTATTTTAC TGTAATATA TCTTTTAGGT  
101 CTAGTCTTAA TATTTAACTT TTTGTCTTAC TTTTAATAGA TTTTATTTGA  
151 GAAAAATTAA TAATTACAAA AAATAAAGG TATATATTCA CATACTTATA  
201 GTACAACTT TGTTTCTATT TATAAGAGA AAAAGAAAT TTACAAAAAA  
251 CAAATATATT TGCTTTCTTT TAATTAGTAG TTTTATTAAG CAAGCTATAG  
301 AAGCTC

**pS211-1 (SEQ ID NO:10)**

1 GAATCCCGTG GTTTAGCAC GGTGCGTCAA TTGTCATATT TGGCTCATTT  
51 ATCTGATTTT TAAACAATTA AGAAGTTATA TGCAATTTTA ACTTTTAAAA  
101 CCGCTTTTAT CATTATTTAT TTTATACAAA ATTACAACGT CGTGAAGGAG  
151 CATCTCGAAC CACGCCACAA CCAAGTGCAC CGTGATTTGT TGACGCAATT  
201 TGGACTTCGT CAAGATCGTG ATTTGGGTTA CATAAATGTA CACCCGTAT  
251 TTAAGAAAAAT AACCTTATTA AATATTGCGC CAAATACTA CGCGTTATGA  
301 TACTATTAGG GTAGGCTTGT GAATTTTACT AAATCGCCCA TCTCGGAATC  
351 TAGGTATTTT CTTATATTAA AAAAAATAAG ATGGGGGCC TCAATTTTTT  
401 ATTTATTAAT ATTTATTTAT TTTTTCAGCA AGATCCCTCC CTTATTTTAT  
451 GAATACCCCT TAATGACTAC ATCTTTATTA TTAATAAGTT TGTCTATAAT  
501 TATGAAGTCA ATCTCTACAT ACATAAAAAA AACATATTAA TTAATAATT  
551 AAAACAAATA TTAATGGAAA GTAATATTAC TAAATTTATA ATTACAAACA  
601 ACATGGAATT GTCACAAAAA AAAAAATAAA AACTAATTAT CCCATAGTTG  
651 GATTAATAAT CATATTGTTA GTATGACTTA AGCTT

**FIG. 3. (continued)**

# pS217-1 (SEQ ID NO:11)

1 AAGCTTTAAA AGGAAGAGAG CCACAATTTT CTTTGACCTT CCTTCTCTCC  
51 TAGCCACTAA GATATACAGT ACTGGTCAAA AAGAGCATAT TTATAGCTCA  
101 AAATTTTGCC TTTTCTGTG GTAAACGTGA TGTCTCTTA CTGGATTCT  
151 TGTTCATAT ATTTACGGGA GAAAAGAGCA ATTTGCATGC TCCTAAATCT  
201 TTTATTTTCT GGTGAAAAAT TGGTCTTTAA TTGGCTGGGA ATTATTTTTT  
251 AGATGCTACA ACCTTGACAA ACACCTAAGA ATATTTTAGT GACAAATGGCT  
301 TGTTCCTTGA GTACTGGTGT TCTGTCTTCT GGTCCTGTGT TCAACGCCAC  
351 AGCCAAAGAG TCTCGTCGTC ATTGCCCTTC GATTGGCACT CTGCAACTTA  
401 AAGATTTAGC ATCCAGAGAA TTCTAGGCA AACCTTGGTA TTATGCATCA  
451 GATCATATTG GTACTAACCA TTGGAATGTT GAACGACTTT CTGTATGTAA  
501 ATCTCTGATA CATTTGCTTC TGTGTTTATA CTGGTGTTT TCATGTTTTT  
551 ATTCTGTGTT TAAATTTTTT GAGATCAAAT CATTATAAG TATTATTCT  
601 AATGATTTTA GGCACAAGTA TCAATCGCTG CTCAGAGATG GTGGGAGAAG  
651 ACCCTTAAAC CCAACATGGT AGAGATCAAT TCAGCAACAC AACTTGTGTA  
701 TTCATTATTA AAAGCTGGTA ATAGATTGGT CATAATTGAC TTCTCTCTC  
751 CTAGCTGTAG AGGTTTCAAG ACTTTACATC CTAAGGTAAG ATATATAGCA  
801 ATCCCCTAAA AAAAAAAAAA AAAAAAAAAA AAACCAACAA CTACATCGTA  
851 ATCCTAAGCA AGTTAGGGTT AACTATATGA ATCATCACTA GACGGATCC

# pS218 (SEQ ID NO:12)

1 AAGCTTAACT TTACTACAT TGCTTTCTTT AGGGAAGCGT CTTCTTAAAT  
51 GACCATCCTC TAAATTTCTC ATGAATCTTC TTCTGTTGTC CACTCTGTTA  
101 TCGCTGAAAC GAAATCTGAA ATTGTCAATG TGCTGACTAT TATCCAATCA  
151 CTCAGTCTCT AATTCATATT TAGATTATCT TGTTCACCAG CCCATACTGA  
201 TTTTATTGTT TTTGGGGTCT AACCTTTCTC TCCGGTAGTC GGTGAGATC  
251 ATGAACCTAT TTCTTGAAT GAGGATATGA CTTTATGGCC TATACTCTTT  
301 TGGTGTCTCA AGGCCTGTCA CCTCTCATCT TTCTCTCAA TTGACTATAG  
351 ACTCTGTAAT ACTGTCTATC TTGGGATCTA CCGTTGTCCT CCAATGTATCA  
401 TATCTTACTC ATAATGCTTC ATTAACATATT TTCTTATTTC CCGCTAACAT  
451 TTATGTCTAT CACTTTATTC TGAAAACTCG AACAAAGACAT TCTTTTCGTT  
501 TTAGATCCCC TTGTCTCCAT CCAGTGGTTC TTCCGGGGAC TTAACGTTCT  
551 CGCTCTCCTA GGGAGGCGAG CCACACTAAG GTAATATTTA TCCCTCTAG  
601 GCTTTCCGTG CCTATCTCT GAGATATTTT TTTTATGCTA ATATTCACAT  
651 CTAATTGTAA TTTTCTAGAG TGCCTCATCT GGGTGCCTCA CAAGAAGAGC  
701 TATTAGCATC TTTGTAATAT CCTTCGGAAA TGTCAACTAA CACAACACAA  
751 TCCATTCAAC ATTTTGGGTT ACTCTAACCT CAGTCGGATA CTAATATCCT  
801 GTCAATTTAT TAACTACAC ATGTTAGCCC CCAATAGGAT ATAACTAAGA  
851 TGGGTGTGGC CAATTTCTACA TACATCTGTT ACTGTTGAAA GTAAGTCGCA  
901 ATGCTTTTAT TTTTCTGCC GAGTTGAAAA TACCGATAAT CTATATTAACT  
951 TGGGTACCTC GTACCTTCTC CATCTTCTCT CTTTACTTTG TTGAAGCTT

FIG. 3. (continued)

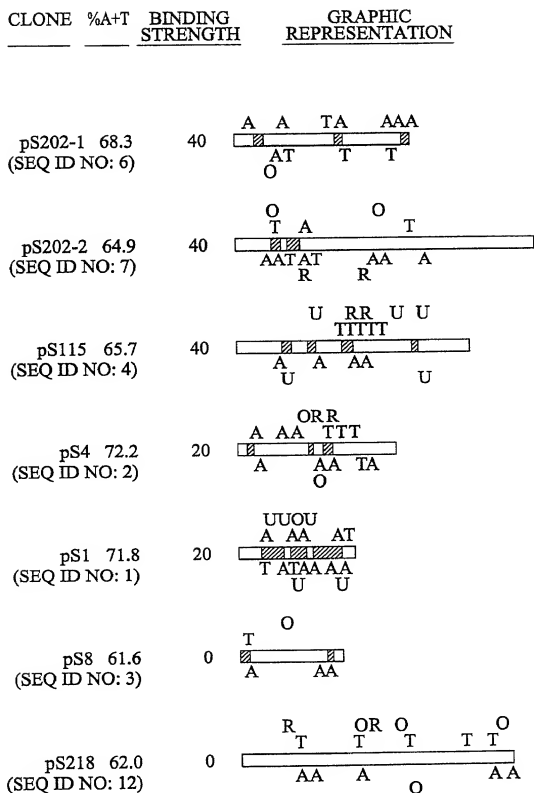
pS220-1 (SEQ ID NO:13)

1 AAGCTTGAAA AAGAAGAATT AAGGCTTGCT TTCTTAATTT TAAAAAATA  
 51 AAAATTATTT TGAACATCT ATACTATATT AAAAGCACGA AAACCCATAC  
 101 GAAATGTCGT TCGCCTTTTT TACCCTTTAA AAATAATTTT ACATTAGACA  
 151 AAATAGTCAT TTACTATTT TTCTTAATAT ATAGGATTTT AAAATTAATT  
 201 TAACTTTGGC TATTAACAT TTTCTTATAA CTTGAAATAT GTAAACTCC  
 251 TAATATTTAG AATTTTAATT AACATAACCA AGGATTTTTA TATCGGTAAT  
 301 AACTCTAATA TGGTATCCAA ATCAGTCTAG AACTCTCTTA CCTCTAATAA  
 351 GTAAAAAGTAC TTCTAATAAA TTCATATACT TTCTCTCTCT TCTCCGATCT  
 401 CTCTTTGCTC TTCTTTTTAT GTATCCTTTC CTCTCTAATA GCCTTTTATG  
 451 AGAAGTAAAC TTTTAGGGTT GGCCCCCCT CCCCCACAA TTATATAGTT  
 501 TCTTACTCAG TTGTTGGAAT ATAATTCAAA TTCTTAAATA ATTGACGGTG  
 551 ACATTGAGTT TTACTTTGTG GAAGAGAATT AGATTCTCGT GTTAGTAAAA  
 601 TCGGTTAGTA ATTGATGATG CATTATTTTT ACTCTATAAT AGAGATGCAA  
 651 TTTTATTTTT GCATTTTGGG ATCAAATGT AATGCAGTCA TATATTGATT  
 701 TCATAAATGT TTGGGATATT GTTGGTTATT TAACTAGAAA TAGACTTCTT  
 751 ATTTTCATATT TATTGTTAAA ATCCTTTATT GGAGATGAAT TATTGTTC  
 801 CCGATTAGAA GTTGATAGTC GCTTTTGTTT TAGAAGAAAT TTTACCGTAG  
 851 ACCAAGTTAA GGAGTTTTAG AAGCACTTTG CATGGGAGCA TTAGTGATG  
 901 TTATGGCTTT ATCAAATATA GGTTTTGAAG ATTCTAGAGAG CCAAGAAAAG  
 951 CTAGAACCCA AGAACTAGGA AGTTAGAGTA ATTCACAATA CCATAACGTG  
 1001 ATATAAACT TTTTATTGTA ACTCAAATCG GTAATATTTT TTGCTTTAGT  
 1051 CTTAATCGAT AAATTATTTT TTATATTGA TTAGTTATAG GAGGCTCACA  
 1101 AAGTTGGGAA TAATTAATAA ATCATATTTT GTATTTGAAC AATTATGAA  
 1151 ATAGTAATTG GTAAAAATC ACTTTAAATT TTATCCCTAT ATCCAGAAGG  
 1201 ATTATGGTGT CTGGCATAGT TGTTTGGAAG ATTGAATCA GGGTAAAGT  
 1251 ATGTTGTAAT TTTTATTTTG TTATAGGCAT TTTTGTGCT TGATTGTTT  
 1301 GTTGTCATTA TATTTTATTA TTTGGAAGTG TATATATATG TTTGATTAAA  
 1351 ATATAGATAA TCAATTTTAT AAGAAATTTG CAACAATTAC ACAAGGATAA  
 1401 AGTCTACAAT ATGCGAGTAA AATTIGATTG AACCTAGGAT GTCATATTTA  
 1451 ATGCATATTT TATTTCAATG TGTTTATTAT ACATCTATTG TATTATATG

FIG. 3. (continued)

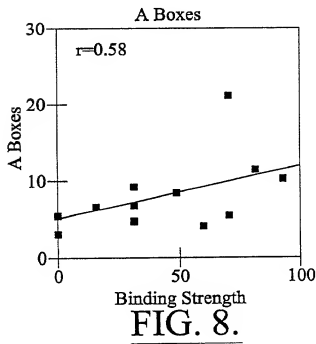
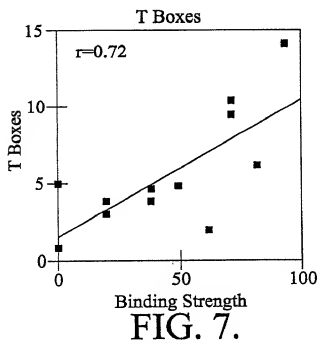
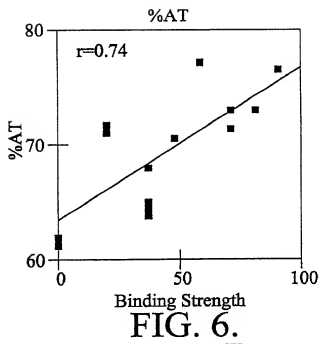
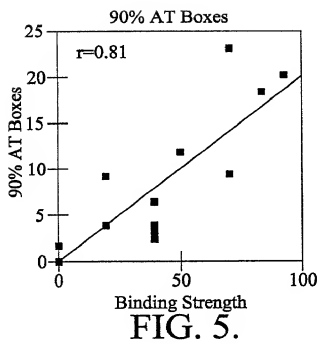
CLONE	%AT	BINDING STRENGTH	GRAPHIC REPRESENTATION
pS116-1 (SEQ ID NO: 5)	76.6	90	
RB7-6 (SEQ ID NO: 20)	73.2	80	
pS211-1 (SEQ ID NO: 10)	71.7	70	
pS220-1 (SEQ ID NO: 13)	73.1	70	
pS226-1 (SEQ ID NO: 9)	77.1	60	
pS205-2 (SEQ ID NO: 8)	71.4	50	
Ps217-1 (SEQ ID NO: 11)	65.2	40	

FIG. 4.



**FIG. 4A.**





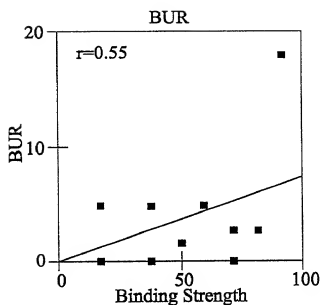


FIG. 9.

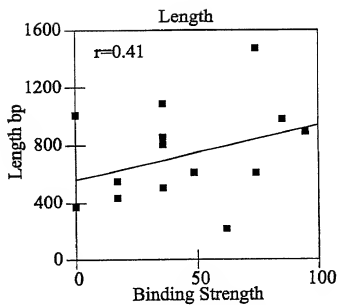


FIG. 10.

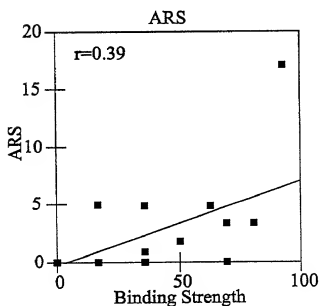


FIG. 11.

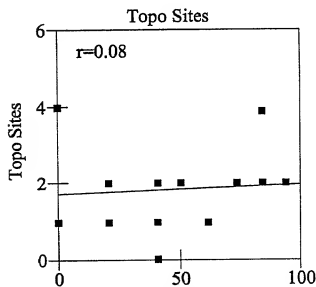


FIG. 12.